



SEQ ID NO:90
3684 nucleotides
DNA
Arabidopsis thaliana

CDS
(501)..(557)

(689)..(818)

(1008)..(1114)

(1194)..(1320)

(1469)..(1576)

(1671)..(1786)

(1858)..(1941)

(2040)..(2108)

(2198)..(2269)

(2352)..(2443)

(2545)..(2672)

(2772)..(2873)

(2965)..(3032)

(3122)..(3181)

agcgattcct tagcagaaag gcgtccatt tctctggcgt aaaccaaagg agatcctga 60

actgtttcct gcaccattgc tcttaaaacc cttctccggc acgaattctt ccaaccctgc 120

ttcaccaccg gaacattgag acaaaatctc gacggtgacg ctgaggttga aaaaaccaat 180

cgaaccgcag acgtaccagg aaccgaacca tgtatcaacg ccattgaaga agaagaaga 240

gaagaaggtg aaaaacgaaa gattgagaat ttgtttgctt tgagcaacca aacctcagga 300

FIG. 19A

aaaaagagtt aaggtgggag tgtctggttc aaccggttta tatccggttc aaattaaacc	360
tcttacagtt aaccgggttt tgtgtttgtg tcgattgttc ataaaagaaa gaagactctt	420
gtcgtcgatt agtgccaaag ttgaaagttg aaaccttttc tcagaatttt ctgctcagtt	480
ctgagttttt ttttcccgcc atg gaa atc gac tcc gag aaa att cac gaa agg	533
Met Glu Ile Asp Ser Glu Lys Ile His Glu Arg	
1 5 10	
aag caa tcc gat tac aat tcg ctg gtacgaactc tattacttta tcgacttgta	587
Lys Gln Ser Asp Tyr Asn Ser Leu	
15	
gtgaaagaca aatgtaatca ttcgtggtgg tgactgtttc tacttataag tgtacgggct	647
agggtttggt atctgattct gagtttttgc aattgaagca g gat gag aga ttc gag	703
Asp Glu Arg Phe Glu	
20	
ata cag aag gag atg tac aga ggt cag caa tac agt cag att tac ttt	751
Ile Gln Lys Glu Met Tyr Arg Gly Gln Gln Tyr Ser Gln Ile Tyr Phe	
25 30 35 40	
gct cgt ctt cat ctc atg aga aca ctt ctc tac tct ctt gct cct act	799
Ala Arg Leu His Leu Met Arg Thr Leu Leu Tyr Ser Leu Ala Pro Thr	
45 50 55	
tgg aaa tct cat ttg cct g gtcagtgcct ttgtttctct catatttagc	848
Trp Lys Ser His Leu Pro	
60	
acaacaacga agagcagttt ttgagaattt tcttgggtta gatataatta ggtgaaatca	908
gtgattttta gggatttttg ctatcttatg gattacagtt gagaaagatt gctagtattg	968
tttaaattat agatctgaat gtgaatttca tttttgcag tg tgt aag gtt ttg	1021
Val Cys Lys Val Leu	
65	
gga ctt gaa aaa gga aaa gaa tgc ata att gtg gga acc ttg ttc aaa	1069
Gly Leu Glu Lys Gly Lys Glu Cys Ile Ile Val Gly Thr Leu Phe Lys	
70 75 80	

FIG. 19B

cac atg aag ctt aaa cct tgt gtt ctc gat gaa tat tct aaa gag	1114
His Met Lys Leu Lys Pro Cys Val Leu Asp Glu Tyr Ser Lys Glu	
85 90 95	
ggttggtttt attaacctct actgtttttt tgagctatgt ctatgctgaa tcaatctgag	1174
tatatttaac ataatgcag agg tca gtt act ccg ctt gtt aaa cca cat aac	1226
Arg Ser Val Thr Pro Leu Val Lys Pro His Asn	
100 105	
ttt atg cat cct gat gat aat ctg atc ctc gaa gac gag agt ggg aga	1274
Phe Met His Pro Asp Asp Asn Leu Ile Leu Glu Asp Glu Ser Gly Arg	
110 115 120 125	
ggt aag ctt gct ggt tcc gca ctt tca cct gcg att tat gtg aca g	1320
Val Lys Leu Ala Gly Ser Ala Leu Ser Pro Ala Ile Tyr Val Thr	
130 135 140	
gtattgcaaa tgggttctta ctgtttttac tgtatgattt tttccttctt tacaatgtgg	1380
caaatcttag agattttgat caagctttcc tctcttaaaa gatgggttct ttaagaaaat	1440
taacgttgaa gcctcccgtg cattgtag gt gtt gtt gtt gca ctg cat ggg	1491
Gly Val Val Val Ala Leu His Gly	
145	
aag gaa act aat gct ggt gaa ttc ttt gtt gag gat gta cta gaa gct	1539
Lys Glu Thr Asn Ala Gly Glu Phe Phe Val Glu Asp Val Leu Glu Ala	
150 155 160	
ggt tta cca cct cag att gag cgg cct atc gat cta c gtaagtctag	1586
Gly Leu Pro Pro Gln Ile Glu Arg Pro Ile Asp Leu	
165 170 175	
ctatgttctc ttccttttgc taacctcatg gctcaatcat ttctataagc aatctctcat	1646
gatacatcca tattgcatct gcag ag gaa gat aaa tat gtc gtg tta ttg	1696
Gln Glu Asp Lys Tyr Val Val Leu Leu	
180 185	
tcg ggc ctt tgt att gga agc aaa tcg gct aat ccc ctg cag ttt cag	1744
Ser Gly Leu Cys Ile Gly Ser Lys Ser Ala Asn Pro Leu Gln Phe Gln	
190 195 200	

FIG. 19C

ctt ctt gtt gac cat ata act ggg cat ctc gga gat gag gag Leu Leu Val Asp His Ile Thr Gly His Leu Gly Asp Glu Glu 205 210 215	1786
gttcaaatct cttacttgc aggtgttca acatatttct ttccttaatt tatactttat	1846
ggtttgaaca g gaa caa ggc ctt gca gca cag ata gtt cat gta gta att Glu Gln Gly Leu Ala Ala Gln Ile Val His Val Val Ile 220 225	1896
gct gga aac tct ttt gaa ttt ccc cgc aaa ctc att aat ggc cag Ala Gly Asn Ser Phe Glu Phe Pro Arg Lys Leu Ile Asn Gly Gln 230 235 240	1941
gtacttataa cttttgttgc tgatatattc tcagatacag ttccagtaat tatctgcccc	2001
agttatgtct tatgatcttt attggttgat cttttag aac ttg gcc tcg aaa gat Asn Leu Ala Ser Lys Asp 245	2057
caa tcg aca ctg tat gag ccc atc aaa gag ctt gat atc atg tta agc Gln Ser Thr Leu Tyr Glu Pro Ile Lys Glu Leu Asp Ile Met Leu Ser 250 255 260 265	2105
cag gtcagttaac tggatctacg tgtgtgttat cgatatctat tgagatgaaa Gln	2158
gttcaaaactc ctgttttttt tttgttgat tgttttttag ata gct gca gga gtt Ile Ala Ala Gly Val 270	2212
tca gta gat atc atg cca ggc acg aat gat cca gct aac ttc gca ttg Ser Val Asp Ile Met Pro Gly Thr Asn Asp Pro Ala Asn Phe Ala Leu 275 280 285	2260
cct cag cag gtctgcaaat acataagaaa cattcaaaat cccgcatttt Pro Gln Gln 290	2309
gtatcgataa ctctgattca taggcccttc tcttttgttc ag cct ctg aat aga Pro Leu Asn Arg	2363

tgt ctt ttc cct gga tct tca cct tat aac acc ttc aga tca tgt aca	2411
Cys Leu Phe Pro Gly Ser Ser Pro Tyr Asn Thr Phe Arg Ser Cys Thr	
295 300 305 310	
aat cct cac tca ttt gat gtc gat aat atc ag gtagtattat tattaatagt	2463
Asn Pro His Ser Phe Asp Val Asp Asn Ile Arg	
315 320	
tgaatacaat ctctctgatt ttacaacgat aaaattcttg ggtttatctg actgaaaacc	2523
tcatatgggg gcattttgca g a ttt ctt gga act tct ggt cag aac atc gat	2575
Phe Leu Gly Thr Ser Gly Gln Asn Ile Asp	
325 330	
gac ctt ggc aag tac tca gag gct aag agc aag ctt gat ttt gtg gaa	2623
Asp Leu Gly Lys Tyr Ser Glu Ala Lys Ser Lys Leu Asp Phe Val Glu	
335 340 345	
aga acg ctg agg tgg aga cat ctt gcc cca act gca cct aat aca ctc g	2672
Arg Thr Leu Arg Trp Arg His Leu Ala Pro Thr Ala Pro Asn Thr Leu	
350 355 360	
gtaagaattc tccttgccct gcaagattac ttttttgaac taagcccata aaaaaatgat	2732
cctttgagtt ctatttggtt ttgattcact tgcgtacag gt tgt tat cct ttc	2785
Gly Cys Tyr Pro Phe	
365	
acc gat aga gac cct ttc ttg att gaa acc tgc ccg cat gtc tac ttc	2833
Thr Asp Arg Asp Pro Phe Leu Ile Glu Thr Cys Pro His Val Tyr Phe	
370 375 380	
gtc ggg aat caa gat aaa tat gac aac cgt ttg ata aag g gtaaaagcac	2883
Val Gly Asn Gln Asp Lys Tyr Asp Asn Arg Leu Ile Lys	
385 390 395	
cttacacaga gattagaaat aacattctct tttgtcaaac atcaggcttt aacttttctt	2943
gggtaaatat gaatgctgca g gg tca gaa ggg cag ctt gtc cgg ttg atc	2993
Gly Ser Glu Gly Gln Leu Val Arg Leu Ile	
400 405	

tgc att cct aag ttc tgt gag acc ggt att gct gtt gcg gtgagtttaa	3042
Cys Ile Pro Lys Phe Cys Glu Thr Gly Ile Ala Val Ala	
410 415 420	
aatttgagca gaatttgaga ccatttacc tcatagattg cagattctaa atctcaaaat	3102
caccatgtct atttcgcag gtg aac cta aga aat ctg gaa tgt cac act tta	3154
Val Asn Leu Arg Asn Leu Glu Cys His Thr Leu	
425 430	
agc ttt agc act cag ata aac caa tca taacattgag ttgctacttt	3201
Ser Phe Ser Thr Gln Ile Asn Gln Ser	
435 440	
ggtagattat ttctgtctt gaagatgtaa tgttgagctt tttcagtaac acactcctat	3261
gttctaacca aatgtttgtt aaaaatcctt ttctttgagt ggaacttcca aatctttgga	3321
tatattggta atgctcattg ttttgccta attttctaaa aatctcgaca cgagttctta	3381
ggtagtcaca taaaggacaa aaagggccga ccagatagtg tcgtggtcgt tggtcagaag	3441
aacgtgaaaa gactgcacaaa ataatcttaa aaaaagcaac aagtgcacag aatctcatgc	3501
aaatgtctct ctctctcttc tcaacggcta tatccatcca cacttattac attataaaat	3561
taattaaatg caataatgta acgcattata ttctccaacg gtccattttc ccgcattttc	3621
ctaacccttc ctttataacg caaaacagtt tcattcttcta cacttaacac tttaatcctc	3681
tct	3684

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(2545)..(2672)

(2772)..(2873)

(2965)..(3032)

(3122)..(3181)

agcgattcct tagcagaaag gcgctccatt tctctggcgt aaaccaaagg agatccttga	60
actgtttcct gcaccattgc tcttaaaacc ctctccggc acgaattctt ccaaccctgc	120
ttcaccaccg gaacattgag acaaaatctc gacggtgacg ctgaggttga aaaaaccaat	180
cgaaccgcag acgtaccagg aaccgaacca tgtatcaacg ccattgaaga agaagaagaa	240
gaagaaggta aaaaacgaaa gattgagaat ttgtttgctt tgagcaacca aacctcagga	300

FIG. 20A

FIG. 20B

cac atg aag ctt aaa cct tgt gtt ctc gat gaa tat tct aaa gag	1114
His Met Lys Leu Lys Pro Cys Val Leu Asp Glu Tyr Ser Lys Glu	
85 90 95	
gttggttttt attaacctct actgtttttt tgagctatgt ctatgctgaa tcaatctgag	1174
tatatttaac ataatgcag agg tca gtt act ccg ctt gtt aaa cca cat aac	1226
Arg Ser Val Thr Pro Leu Val Lys Pro His Asn	
100 105	
ttt atg cat cct gat gat aat ctg atc ctc gaa gac gag agt ggg aga	1274
Phe Met His Pro Asp Asp Asn Leu Ile Leu Glu Asp Glu Ser Gly Arg	
110 115 120 125	
gtt aag ctt gct ggt tcc gca ctt tca cct gcg att tat gtg aca g	1320
Val Lys Leu Ala Gly Ser Ala Leu Ser Pro Ala Ile Tyr Val Thr	
130 135 140	
gtattgcaaa tgggttctta ctgtttttac tgtatgattt tttccttctt tacaatgtgg	1380
caaatcttag agattttgat caagctttcc tctcttaaaa gatgggttct ttaagaaaat	1440
taacgttgaa gcctcccgtag cattgtag gt gtt gtt gtt gca ctg cat ggg	1491
Gly Val Val Val Ala Leu His Gly	
145	
aag gaa act aat gct ggt gaa ttc ttt gtt gag gat gta cta gaa gct	1539
Lys Glu Thr Asn Ala Gly Glu Phe Phe Val Glu Asp Val Leu Glu Ala	
150 155 160	
ggt tta cca cct cag att gag cgg cct atc gat cta c gtaagtctag	1586
Gly Leu Pro Pro Gln Ile Glu Arg Pro Ile Asp Leu	
165 170 175	
ctatgttctc ttccttttgc taacctcatg gctcaatcat ttctataagc aatctctcat	1646
gatacatcca tattgcatct gcag ag gaa gat aaa tat gtc gtg tta ttg	1696
Gln Glu Asp Lys Tyr Val Val Leu Leu	
180 185	
tcg ggc ctt tgt att gga agc aaa tcg gct aat ccc ctg cag ttt cag	1744
Ser Gly Leu Cys Ile Gly Ser Lys Ser Ala Asn Pro Leu Gln Phe Gln	
190 195 200	

ctt ctt gtt gac cat ata act ggg cat ctc gga gat gag gag Leu Leu Val Asp His Ile Thr Gly His Leu Gly Asp Glu Glu 205 210 215	1786
gttcaaactc cttaacttgc aggttggtca acatatttct ttccttaatt tatactttat	1846
ggtttgaaca g gaa caa ggc ctt gca gca cag ata gtt cat gta gta att Glu Gln Gly Leu Ala Ala Gln Ile Val His Val Val Ile 220 225	1896
gct gga aac tct ttt gaa ttt ccc cgc aaa ctc att aat ggc cag Ala Gly Asn Ser Phe Glu Phe Pro Arg Lys Leu Ile Asn Gly Gln 230 235 240	1941
gtacttataa cttttgttgc tgatatattc tcagatacag ttccagtaat tatctgcccc	2001
agttatgtct tatgatcttt attggttgat cttttag aac ttg gcc tcg aaa gat Asn Leu Ala Ser Lys Asp 245	2057
caa tcg aca ctg tat gag ccc atc aaa gag ctt gat atc atg tta agc Gln Ser Thr Leu Tyr Glu Pro Ile Lys Glu Leu Asp Ile Met Leu Ser 250 255 260 265	2105
cag gtcagttaac tggatctacg tgtgtgttat cgatatctat tgagatgaaa Gln	2158
gttcaaactc ctgttttttt ttttgtggat tgtttttag ata gct gca gga gtt Ile Ala Ala Gly Val 270	2212
tca gta gat atc atg cca ggc acg aat gat cca gct aac ttc gca ttg Ser Val Asp Ile Met Pro Gly Thr Asn Asp Pro Ala Asn Phe Ala Leu 275 280 285	2260
cct cag cag gtctgcaa atcataagaaa cattcaaaat cccgcatttt Pro Gln Gln 290	2309
gtatcgataa ctctgattca taggcccttc tcttttggtc ag cct ctg aat aga Pro Leu Asn Arg	2363

FIG. 20D

tgt ctt ttc cct gga tct tca cct tat aac acc ttc aga tca tgt aca Cys Leu Phe Pro Gly Ser Ser Pro Tyr Asn Thr Phe Arg Ser Cys Thr 295 300 305 310	2411
aat cct cac tca ttt gct gtc gat aat atc ag gtatgattat tattaatagt Asn Pro His Ser Phe Ala Val Asp Asn Ile Arg 315 320	2463
tgaatacaat ctctctgatt ttacaacgat aaaattcttg ggtttatctg actgaaaacc	2523
tcatatgggg gcattttgca g a ttt ctt gga act tct ggt cag aac atc gat Phe Leu Gly Thr Ser Gly Gln Asn Ile Asp 325 330	2575
gac ctt ggc aag tac tca gag gct aag agc aag ctt gat ttt gtg gaa Asp Leu Gly Lys Tyr Ser Glu Ala Lys Ser Lys Leu Asp Phe Val Glu 335 340 345	2623
aga acg ctg agg tgg aga cat ctt gcc cca act gca cct aat aca ctc g Arg Thr Leu Arg Trp Arg His Leu Ala Pro Thr Ala Pro Asn Thr Leu 350 355 360	2672
gtaagaattc tccttgccct gcaagattac ttttttgaac taagcccata aaaaaatgat	2732
cctttgagtt ctatttggtt ttgattcact tgcgtacag gt tgt tat cct ttc Gly Cys Tyr Pro Phe 365	2785
acc gat aga gac cct ttc ttg att gaa acc tgc ccg cat gtc tac ttc Thr Asp Arg Asp Pro Phe Leu Ile Glu Thr Cys Pro His Val Tyr Phe 370 375 380	2833
gtc ggg aat caa gat aaa tat gac aac cgt ttg ata aag g gtaaaagcac Val Gly Asn Gln Asp Lys Tyr Asp Asn Arg Leu Ile Lys 385 390 395	2883
cttacacaga gattagaaat aacattctct ttgtcaaac atcaggcttt aacttttctt	2943
gggtaaatat gaatgctgca g gg tca gaa ggg cag ctt gtc cgg ttg atc Gly Ser Glu Gly Gln Leu Val Arg Leu Ile 400 405	2993

tgc att cct aag ttc tgt gag acc ggt att gct gtt gcg gtgagtttaa	3042
Cys Ile Pro Lys Phe Cys Glu Thr Gly Ile Ala Val Ala	
410 415 420	
aatttgagca gaatttgaga ccatttaccc tcatagattg cagattctaa atctcaaaat	3102
caccatgtct atttcgcag gtg aac cta aga aat ctg gaa tgt cac act tta	3154
Val Asn Leu Arg Asn Leu Glu Cys His Thr Leu	
425 430	
agc ttt agc act cag ata aac caa tca taacattgag ttgctacttt	3201
Ser Phe Ser Thr Gln Ile Asn Gln Ser	
435 440	
ggtagattat ttcctgtctt gaagatgtaa tgttgagctt tttcagtaac acactcctat	3261
gttctaacca aatgtttgtt aaaaatcctt tttcttgagt ggaacttcca aatctttgga	3321
tatattggta atgctcattg ttttgccta attttctaaa aatctcgaca cgagttctta	3381
ggtagtcaca taaaggacaa aaagggccga ccagatagtg tcgtggtcgt tggtcagaag	3441
aacgtgaaaa gactgcaaaa ataatcttaa aaaaagcaac aagtgcacag aatctcatgc	3501
aaatgtctct ctctctcttc tcaacggcta tatccatcca cacttattac attataaaat	3561
taattaaatg caataatgta acgcattata ttctccaacg gtccattttc ccgcatttcc	3621
ctaacctttc ctttataacg caaaacagtt tcatcttcta cacttaacac tttaatcctc	3681
tct	3684